



#4

Sarjeet S.  
Ross, Linda S.

The Regents of the University of California

<120> Use of Insect Cell Membrane Transporters as Novel  
Target Sites for Insecticides

<130> 023070-093800US

<140> US 09/815,923

<141> 2001-03-23

<160> 20

<170> PatentIn Ver. 2.1

<210> 1

<211> 5554

<212> DNA

<213> Manduca sexta

<220>

<223> vesicular acetylcholine transporter

<400> 1

gagactcagg	ttccgaagtc	ctatccgagg	gtcgacgagt	cctgttcgtg	gacgccgcgt	60
aaatgtactg	actactgtga	gcgacgcgag	tgtaccatcc	gcaacgtaac	cagctctaga	120
agatgaacac	agatccccag	cagttagaat	attaacgtga	tacacaagta	gttaacatgg	180
cggaggggacc	acagacaata	tggcagaaga	tcgacaactc	catcatcccc	gtcataaacc	240
tggaggtgcg	ggaggtccgg	gagatattat	gggagaagat	acaggaaccc	acctcacaga	300
ggaagatcat	cctggtgata	gtgtccatag	cgctgctatt	agacaacatg	ttgtatatgg	360
tgatcgtgcc	tatcatcccc	gactacttga	ggtatatagg	cgcatgggga	gaggcaggct	420
acgaccatgt	cgttaccttg	ccgcccatac	gagagggtaa	caggaccatc	ataccgacca	480
agattatacc	cgcgtcacac	catggtcagg	actctgcgac	gggagtgtct	ttcgcgtcca	540
aagctatagt	gcagctcatg	ataaacctt	tctccggtgc	cttaattgac	cgcatagggt	600
acgatatacc	catgatgata	ggactcataa	taatgttctt	atcgacctca	atattcgcgt	660
gcggtcggag	ttacagcatg	ttgttcttcg	cgaggagtct	ccagggagta	ggatcggcgt	720
ttgctgatac	ttcagggctg	gccatgattg	ctgaccgggt	tactgaagaa	agtgagcgct	780
caaaggctct	tggaaattgcc	ctcgcattta	taagtttcgg	aagccttgta	gcgccacctt	840
ttggaggtgc	tttgtatcag	tttgccggta	aagaagtacc	gtttcttatt	ctcgcctctga	900
tatctttaat	ggatggattc	atgctgctat	tggtaatgaa	accaattaaa	acgcagatga	960
aagaagcgaa	ccaaccgaag	ccagctggca	ctccgatatg	gaaactcctc	atggaccctg	1020
atatcgagtc	atgtgctgga	gctctcatga	tgtctaacgc	tgctttgggt	ttcctcgagc	1080
ctacaatttc	ctcctggatg	gaagataact	tgaccaaaga	caattggaag	attggcatga	1140
tatggctacc	agctttcttc	ccgcacgttc	ttggggtaat	catcacagta	aagatggcaa	1200
agaaataccc	acaacaacaa	tggtgatgag	ctgctgggtg	attggcttta	gaaggattgt	1260
gctgtttcat	tattccgttc	gcgagttcgt	acaaaatgct	catgatacct	atttgcggca	1320
tctgtttcgg	gatcgcgttg	attgacactg	ctctactgcc	cacctggggt	tacctggtcg	1380
atgttcggta	cgtttctgtg	tacggaagca	tctacgcaat	cgctgatata	tcatattcat	1440
tcgcgtatgc	tgtggggccg	attatagcag	gagaagtggg	cgaagccatt	ggcttcaactg	1500
ctctgaatct	cctaattgct	ttcagcaacc	tctgttatgc	cccagtactt	atgtacctca	1560
ggcacatcta	cgactttaaa	ccatttgaga	acgaagcaaa	tattctcatg	tctgaccgcg	1620
cggataaaga	ataccaaacg	tacagcatgc	aagatcagag	gcccgtcaac	ggtgaataca	1680
aaaaccattt	ggaatattcc	aacgtgtctg	gacaagtggc	agcaacgcag	gagtcgaatg	1740
tggacgccgc	gcagactggc	tactcatagc	accagtcgta	tcagggggat	tatcagaact	1800
acagccaggc	tacgagcagg	agtaccagca	ccaaccggag	tacaaccagc	cgccgcagtt	1860
gcctgccccg	ccgcagcccc	cgccatagcaa	tccgttccgc	gcaggcacgg	cagcggctcc	1920
cgcaccccg	cccgcgccag	ccccgcctgc	tcccaccatc	aagaacccgt	tccggcaagg	1980
cttctaaatt	ttattcagtg	ttgttgtcga	tatttttgaa	tttacttggt	gtttaattat	2040

aaagttctca	ggtaatgcct	tcgatcactg	agccgcgtca	catcggcggc	gggttttagtc	2100
tctgttaggt	gtctattaga	tgtgcttaaa	ctgtagttgt	gcgagtgatg	tacgtagact	2160
caccaggtaa	tgtgaacctg	ccgggcccta	tgtacaccac	tccagctggt	ttcttggtga	2220
tcttgtagctg	ttctaaaact	gttatgtctt	ctgatataata	agtataacaa	tgtgtaagta	2280
ataataagaa	atatagcggc	gtaaattctcg	atgtacactc	gaaatagaca	tgaaattctt	2340
aaagatatat	cgtttggggt	gtatatagat	acattgtata	aacgtatata	ctggcacacg	2400
attcacgttg	cactaggtaa	gggcctaaga	aatatatttatt	ggtgaaatct	tggcacttac	2460
gggcatttta	atgatctcgc	ttttgtgtaa	cttgatgtga	agctacatag	gtgcgtggga	2520
catagattgt	gggtggaatt	tattataaatt	atatttagatg	acgtcaagcg	ttggacgtgc	2580
gacagcgacg	caggccttgg	tgacgtaatc	aagtccttcac	aaactgcgaa	atatcataca	2640
attgctgtgt	cactatcgct	acgtcattga	ctcgacgtta	ggactacaaa	tggtagtaca	2700
tactacgata	taactgatta	actattttaa	tgaaagtatc	aacatacaaa	ttctgactac	2760
aatctatact	aagctcagaa	ttgtaattat	gtatgtgtca	ttatatTTTT	agacgtacta	2820
taagatatttt	cctatgctat	atcagcaata	ttagtgtacg	gcttcataat	tattctatat	2880
caatagttgt	aggttagtat	caacttgtga	taagttgcaa	ccaagtaacg	aaacatatca	2940
ggatcttttg	atccacgtaa	cttaagttag	agtaatgagg	taagtgata	agtggtagta	3000
aggccacgtt	ttagctttaa	atcaggtaca	tcgatttaac	gtttgggtggg	atgatatcgt	3060
atttcttggt	tagagtcgga	aattaacatt	atagctactt	gcaaaaagta	tgactgaaga	3120
atggaagggt	caatatatac	taatacatat	caaataaaga	agaaatgtta	tgaaaatgtg	3180
agggaaagaa	actataacga	tattggaaat	ttcgtatggt	aatataactt	atataacaga	3240
atttgtttgt	tataaaatct	aatgaaagag	taaattagat	tagagaatgt	ttcaatgata	3300
ttagaattct	acaaaaacct	actactaatc	aaactttatat	acctccatta	ggtaagttaa	3360
gatctcatcc	caccgaaccg	tttacaacac	ggaagattca	attcaattgt	aaagtaattg	3420
tagaagatat	cgcgacgagc	ccgacatgtc	aattgaacga	atgtataaag	taaaacttta	3480
cgtgtaatat	atggatattt	aaaattatta	tgtacacatt	cgtttgaacc	acgctggcac	3540
cgcgcgggtc	ccaaccgctt	tagttcagtg	tgatgggtgt	cctttcatta	gactagagac	3600
aggcaggagg	cattgtatct	ggtggagacc	gtcatgcctg	gcgatcagct	gtccaagact	3660
gcaccaagtg	acaggggtca	cgatcctcag	cattgaggga	aagattagag	agagagagag	3720
agagagagat	acgccattcc	aacatgtaaa	gcataacagg	tctgtacaag	gagagacca	3780
taatgtttac	catgacacat	actttgtgtg	atacgctaaa	tacttctagt	cgagtgtag	3840
cggaaagctc	aaagttgatg	ctcatgacaa	aggggtactt	ggtgtaacca	acattagata	3900
atgaattgggt	aatactaact	tcaaggatat	aagacatgaa	tcacgtaatg	aataacgatt	3960
caacacttta	gaaccgatat	ggatttttct	atttatccac	tctgcgaca	aggcgtttga	4020
caactgggtca	tactatattt	ttcgttgtcg	cactgttagc	agaacatgc	acaagatatt	4080
tcagacctgg	tttcgcacta	aacgtgattg	aaacgagaaa	tctatttgga	tgtttatgaa	4140
aggatattca	tcacaaattc	ctaaggtcac	aaaatttggt	tttggttaag	aagaaattta	4200
tacctagcct	gcaaagtaca	atagcatttg	tagttcagac	tgtctgcaca	tcgtattggt	4260
tcgcgcactg	cacttctaca	ttatgattaa	tgcgtgatg	atcgctcattg	agcaatttaa	4320
aaaaaatgaa	gtaagaaggg	gtccttatta	tatatatctc	agagcatctt	gtcttttttc	4380
tttcaggatg	gcagaagtat	tataatctta	ttcctttttt	ttatatcgga	aattttattgt	4440
agtgtaaata	ttgaagaatt	atgatatttt	ctccattttat	tttctataag	gaaatattgt	4500
attataatga	tattcctaaa	atatttgcac	tcatttttta	ataatatata	ttaatatcaa	4560
aatcgtgcac	acaactaaat	gacgaatcta	taaacctttt	aaacctctga	aacaatatta	4620
atgttgaaacg	ataaatatac	aataaaccac	gagagcttaa	ataagctctg	ttataaagcc	4680
accgcactca	ctttattggt	tgttgtttta	tatttacctt	tccattaaag	tcaaagtgtg	4740
ctttatatatt	aatgtgatat	atattttttt	tatattgctt	gattgaggta	gtcagcgcat	4800
taagaacctt	atttctctag	tgggttccct	acgatagccg	tgctgtaatg	taacaattga	4860
cgtaaaccgc	cgttgtataa	cgaccgttat	ataacgacgt	cgctatccta	gcaacctatg	4920
cttagatact	tttgtatatt	ttaatatgta	acctaatttt	cgcatatttc	tatatataag	4980
tattttcaac	atataataat	gtatattgtg	taacggactc	tccgtgtata	taaggataga	5040
gtcaattttc	ttgtcaaat	ctcccgaat	tcaatttaatt	agtagtgtgt	gaagtgtaca	5100
agtatgatta	aggatgtata	ttgctgtgta	tattgataag	ctaagggtata	tgttgctctg	5160
ttctatagcc	ttaccttcac	catctattcc	ggttctatat	tcggttaaat	acttcgatta	5220
taaataatctg	ttaccgccta	gtgttatgtc	gtaaatctgg	tgatttaatt	tttgggtattt	5280
gtatctaata	ttgcgtcatt	ttgctagtgg	agttttgctt	cctctcttct	ctatgttaag	5340
gtgtatattt	ctttaacaat	caacatacac	gagcgatgtt	caggaagtat	gttgtgattg	5400
ggtaacatat	tctatttagta	tgtgcaatta	tgtgacgta	cttattactg	tatatgtgtg	5460
ttctgttgtg	aggggaatta	aaattgacat	tggtaaaaaa	aaaaaaaaaa	aaaaaaaaaa	5520
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaa			5554

<210> 2  
 <211> 619  
 <212> PRT  
 <213> Manduca sexta

<220>  
 <223> vesicular acetylcholine transporter

<400> 2  
 Met Ala Glu Gly Pro Gln Thr Ile Trp Gln Lys Ile Asp Asn Ser Ile  
   1                  5                  10                  15  
 Ile Pro Val Ile Asn Leu Glu Val Arg Glu Val Arg Glu Ile Leu Trp  
                   20                  25                  30  
 Glu Lys Ile Gln Glu Pro Thr Ser Gln Arg Lys Ile Ile Leu Val Ile  
           35                  40                  45  
 Val Ser Ile Ala Leu Leu Leu Asp Asn Met Leu Tyr Met Val Ile Val  
       50                  55                  60  
 Pro Ile Ile Pro Asp Tyr Leu Arg Tyr Ile Gly Ala Trp Gly Glu Ala  
   65                  70                  75                  80  
 Gly Tyr Asp His Val Val Thr Leu Pro Pro Ile Arg Glu Gly Asn Arg  
                   85                  90                  95  
 Thr Ile Ile Pro Thr Lys Ile Ile Pro Ala Ser His His Gly Gln Asp  
                   100                  105                  110  
 Ser Ala Thr Gly Val Leu Phe Ala Ser Lys Ala Ile Val Gln Leu Met  
       115                  120                  125  
 Ile Asn Pro Phe Ser Gly Ala Leu Ile Asp Arg Ile Gly Tyr Asp Ile  
   130                  135                  140  
 Pro Met Met Ile Gly Leu Ile Ile Met Phe Leu Ser Thr Ser Ile Phe  
  145                  150                  155                  160  
 Ala Cys Gly Arg Ser Tyr Ser Met Leu Phe Phe Ala Arg Ser Leu Gln  
           165                  170                  175  
 Gly Ile Gly Ser Ala Phe Ala Asp Thr Ser Gly Leu Ala Met Ile Ala  
       180                  185                  190  
 Asp Arg Phe Thr Glu Glu Ser Glu Arg Ser Lys Ala Leu Gly Ile Ala  
       195                  200                  205  
 Leu Ala Phe Ile Ser Phe Gly Ser Leu Val Ala Pro Pro Phe Gly Gly  
   210                  215                  220  
 Ala Leu Tyr Gln Phe Ala Gly Lys Glu Val Pro Phe Leu Ile Leu Ala  
  225                  230                  235                  240  
 Leu Ile Ser Leu Met Asp Gly Phe Met Leu Leu Leu Val Met Lys Pro  
           245                  250                  255  
 Ile Lys Thr Gln Met Lys Glu Ala Asn Gln Pro Lys Pro Ala Gly Thr  
       260                  265                  270

Pro Ile Trp Lys Leu Leu Met Asp Pro Tyr Ile Ala Val Cys Ala Gly  
 275 280 285  
 Ala Leu Met Met Ser Asn Ala Ala Leu Ala Phe Leu Glu Pro Thr Ile  
 290 295 300  
 Ser Ser Trp Met Glu Asp Asn Leu Thr Lys Asp Asn Trp Lys Ile Gly  
 305 310 315 320  
 Met Ile Trp Leu Pro Ala Phe Phe Pro His Val Leu Gly Val Ile Ile  
 325 330 335  
 Thr Val Lys Met Ala Lys Lys Tyr Pro Gln Gln Gln Trp Leu Met Ala  
 340 345 350  
 Ala Gly Gly Leu Ala Leu Glu Gly Leu Cys Cys Phe Ile Ile Pro Phe  
 355 360 365  
 Ala Ser Ser Tyr Lys Met Leu Met Ile Pro Ile Cys Gly Ile Cys Phe  
 370 375 380  
 Gly Ile Ala Leu Ile Asp Thr Ala Leu Leu Pro Thr Leu Gly Tyr Leu  
 385 390 395 400  
 Val Asp Val Arg Tyr Val Ser Val Tyr Gly Ser Ile Tyr Ala Ile Ala  
 405 410 415  
 Asp Ile Ser Tyr Ser Phe Ala Tyr Ala Val Gly Pro Ile Ile Ala Gly  
 420 425 430  
 Glu Val Val Glu Ala Ile Gly Phe Thr Ala Leu Asn Leu Leu Ile Ala  
 435 440 445  
 Phe Ser Asn Leu Leu Tyr Ala Pro Val Leu Met Tyr Leu Arg His Ile  
 450 455 460  
 Tyr Asp Phe Lys Pro Phe Glu Asn Glu Ala Asn Ile Leu Met Ser Asp  
 465 470 475 480  
 Pro Pro Asp Lys Glu Tyr Gln Thr Tyr Ser Met Gln Asp Gln Arg Pro  
 485 490 495  
 Val Asn Gly Glu Tyr Lys Asn His Leu Glu Tyr Ser Asn Val Ser Gly  
 500 505 510  
 Gln Val Ala Ala Thr Gln Glu Ser Asn Val Asp Ala Ala Gln Thr Gly  
 515 520 525  
 Tyr Ser Tyr Asp Gln Ser Tyr Gln Gly Asp Tyr Gln Asn Tyr Ser Gln  
 530 535 540  
 Ala Thr Ser Arg Ser Thr Ser Thr Asn Arg Ser Thr Thr Ser Arg Gly  
 545 550 555 560  
 Ser Cys Leu Pro Ser Arg Ser Pro Arg Leu Ala Ile Arg Ser Ala Gln  
 565 570 575  
 Ala Arg Gln Arg Leu Pro His Pro Arg Pro Arg Gln Pro Arg Leu Leu  
 580 585 590

Pro Pro Ser Arg Thr Arg Ser Gly Lys Ala Ser Lys Phe Tyr Ser Val  
 595 600 605

Leu Leu Ser Ile Phe Leu Asn Leu Leu Val Val  
 610 615

<210> 3  
 <211> 1764  
 <212> DNA  
 <213> Manduca sexta  
 <220>  
 <223> serotonin transporter

<400> 3  
 atgccgccgt cggacgcgcc gccgcgccccc accgcgccac ctctgatct tcttgctacc 60  
 accgctcaga aaagccgttc ggtggtggtg tcgcttacgc cggcgcggca gcgcgagacc 120  
 tgggcgaaga aggcagagtt cctgctggcg gtggtgggat tcgcagtggga tcttggtaac 180  
 gtgtggcgat tccccacat ctgttaccag aatggaggcg gtgcgttcct gatcccgta 240  
 tgcgttatgc tgctgtttgg cgggctgccg ctgttcttcc tggaactggc gctggggccag 300  
 taccaccgct gcggctgcct cactctctgg aaacggatct gccccgcgct taaagggtgtc 360  
 ggctatgcca tctgcatgat cgacatctac atgggcatgt actacaacac gatcatcgga 420  
 tgggcggtgt attacctgat cgcttctctc gcgtctataa actctgtgct gccatggacc 480  
 agctgcgaca acgagtggaa cacgccgtg tgcacgcggc tcacctcacc tcagactaat 540  
 cctaactctt ctacaccggc gaaggagttc ttcgaacgta atgtattgga gcagcacaag 600  
 tctaaccggc tggatgacat ggggccgatc aagccgtcgc tggctctgtg tgtgttcggg 660  
 gtctttgtcc tcgtctactt ctcttctgtg aaaggagtca ggagtgtgtg caagggtggtg 720  
 tgggtgacag ctctggcccc gtacgtggtg ctgctgattc tgctggcgag aggcgtcacg 780  
 cttccaggag cgacggaggg catagctac taccttacct cagagtggca caaattgcaa 840  
 aactctaagg tatggattga cgcggcatcc cagatcttct tctcgctcgg tcccgggttc 900  
 ggaaccctac tggcgtcttc cagctacaac aagtccaaca acaactgcta cagggacgcg 960  
 ctcatcactt cttctatcaa ctgcttgacc agcttccttg ctgggttctgt cattttctcg 1020  
 gttttggggt acatggcgca cgttcagaac aagagcatcg aggaggttgg cctcgaaggc 1080  
 cctggactgg tgttcacgtg gtaccccgag gccatcgcca ccatgaccgg ctccgtgttc 1140  
 tgggccatca tcttcttctc catgcttatt accctgggac ttgacagtac ttttgagggt 1200  
 cttgaggcag tcaccacggc tctttgcgac gaatatcttc gagtgtagg cagacatcgc 1260  
 gaagtatttg tggctgtact gcttctgttc atctatatatt gcgctctgcc caccaccaca 1320  
 tacggtggtg tatacctcgt agacctactc aatgtgtatg gccctggatt ggcgattcta 1380  
 ttcgtggtat ttgctgaggc tgccggcggt tctgtgggtgt atggcgctga ccggttctct 1440  
 gaagatgtga ggaccatgct ggggcacacc cctggatggg tctggaggac ctgttggtct 1500  
 tacatcagtc ccgtattctt gctgggtgctg ttcgtgttct ccgttctggc acacgaggag 1560  
 atgctcggcg gggaatacac ctatccctca tgggtctatca ccgtaggctg ggtgatgacc 1620  
 ggcaccaccg tctcgtgcat tctcttttac attatctaca aactgctcat cactcctggc 1680  
 aattgcatca accgcatcaa gacaatccaa cgtccggaag tgacgtcgat acctccagcg 1740  
 gactctaccc tatgcaacct gtga 1764

<210> 4  
 <211> 587  
 <212> PRT  
 <213> Manduca sexta  
 <220>  
 <223> serotonin transporter

<400> 4  
 Met Pro Pro Ser Asp Ala Pro Pro Ala Pro Thr Ala Pro Pro Pro Asp  
 1 5 10 15

Leu Pro Ala Thr Thr Ala Gln Lys Ser Arg Ser Val Val Val Ser Leu  
                     20                    25                    30  
 Thr Pro Ala Arg Gln Arg Glu Thr Trp Ala Lys Lys Ala Glu Phe Leu  
                     35                    40                    45  
 Leu Ala Val Val Gly Phe Ala Val Asp Leu Gly Asn Val Trp Arg Phe  
                     50                    55                    60  
 Pro Tyr Ile Cys Tyr Gln Asn Gly Gly Gly Ala Phe Leu Ile Pro Tyr  
                     65                    70                    75                    80  
 Cys Val Met Leu Leu Phe Gly Gly Leu Pro Leu Phe Phe Leu Glu Leu  
                     85                    90                    95  
 Ala Leu Gly Gln Tyr His Arg Cys Gly Cys Leu Thr Leu Trp Lys Arg  
                     100                    105                    110  
 Ile Cys Pro Ala Leu Lys Gly Val Gly Tyr Ala Ile Cys Met Ile Asp  
                     115                    120                    125  
 Ile Tyr Met Gly Met Tyr Tyr Asn Thr Ile Ile Gly Trp Ala Val Tyr  
                     130                    135                    140  
 Tyr Leu Ile Ala Ser Leu Ala Ser Ile Asn Ser Val Leu Pro Trp Thr  
                     145                    150                    155                    160  
 Ser Cys Asp Asn Glu Trp Asn Thr Pro Leu Cys Thr Pro Val Thr Ser  
                     165                    170                    175  
 Pro Gln Thr Asn Pro Asn Ser Ser Thr Pro Ala Lys Glu Phe Phe Glu  
                     180                    185                    190  
 Arg Asn Val Leu Glu Gln His Lys Ser Asn Gly Leu Asp Asp Met Gly  
                     195                    200                    205  
 Pro Ile Lys Pro Ser Leu Ala Leu Cys Val Phe Gly Val Phe Val Leu  
                     210                    215                    220  
 Val Tyr Phe Ser Leu Trp Lys Gly Val Arg Ser Ala Gly Lys Val Val  
                     225                    230                    235                    240  
 Trp Val Thr Ala Leu Ala Pro Tyr Val Val Leu Leu Ile Leu Leu Ala  
                     245                    250                    255  
 Arg Gly Val Thr Leu Pro Gly Ala Thr Glu Gly Ile Arg Tyr Tyr Leu  
                     260                    265                    270  
 Thr Pro Glu Trp His Lys Leu Gln Asn Ser Lys Val Trp Ile Asp Ala  
                     275                    280                    285  
 Ala Ser Gln Ile Phe Phe Ser Leu Gly Pro Gly Phe Gly Thr Leu Leu  
                     290                    295                    300  
 Ala Leu Ser Ser Tyr Asn Lys Phe Asn Asn Asn Cys Tyr Arg Asp Ala  
                     305                    310                    315                    320  
 Leu Ile Thr Ser Ser Ile Asn Cys Leu Thr Ser Phe Leu Ala Gly Phe  
                     325                    330                    335

Val Ile Phe Ser Val Leu Gly Tyr Met Ala His Val Gln Asn Lys Ser  
                   340                                  345                                  350  
 Ile Glu Glu Val Gly Leu Glu Gly Pro Gly Leu Val Phe Ile Val Tyr  
                   355                                  360                                  365  
 Pro Glu Ala Ile Ala Thr Met Thr Gly Ser Val Phe Trp Ala Ile Ile  
                   370                                  375                                  380  
 Phe Phe Leu Met Leu Ile Thr Leu Gly Leu Asp Ser Thr Phe Gly Gly  
                   385                                  390                                  395                                  400  
 Leu Glu Ala Val Thr Thr Ala Leu Cys Asp Glu Tyr Pro Arg Val Leu  
                                   405                                  410                                  415  
 Gly Arg His Arg Glu Val Phe Val Ala Val Leu Leu Leu Phe Ile Tyr  
                                   420                                  425                                  430  
 Ile Cys Ala Leu Pro Thr Thr Thr Tyr Gly Gly Val Tyr Leu Val Asp  
                   435                                  440                                  445  
 Leu Leu Asn Val Tyr Gly Pro Gly Leu Ala Ile Leu Phe Val Val Phe  
                   450                                  455                                  460  
 Ala Glu Ala Ala Gly Val Cys Trp Val Tyr Gly Val Asp Arg Phe Ser  
                   465                                  470                                  475                                  480  
 Glu Asp Val Arg Thr Met Leu Gly His Thr Pro Gly Trp Phe Trp Arg  
                                   485                                  490                                  495  
 Thr Cys Trp Ser Tyr Ile Ser Pro Val Phe Leu Leu Val Leu Phe Val  
                                   500                                  505                                  510  
 Phe Ser Val Leu Ala His Glu Glu Met Leu Gly Gly Glu Tyr Thr Tyr  
                   515                                  520                                  525  
 Pro Ser Trp Ser Ile Thr Val Gly Trp Val Met Thr Gly Thr Thr Val  
                   530                                  535                                  540  
 Ser Cys Ile Pro Leu Tyr Ile Ile Tyr Lys Leu Leu Ile Thr Pro Gly  
                   545                                  550                                  555                                  560  
 Asn Cys Ile Asn Arg Ile Lys Thr Ile Gln Arg Pro Glu Val Thr Ser  
                                   565                                  570                                  575  
 Ile Pro Pro Ala Asp Ser Thr Leu Cys Asn Leu  
                   580                                  585

<210> 5  
 <211> 1671  
 <212> DNA  
 <213> Manduca sexta

<220>  
 <223> proline transporter

<400> 5  
 atgtctggtg ctacgcaaga ccgatgggga agtcagctag aatatttgct atcatgtttg 60  
 ggatacgccg ttggcatcgg gaacctatgg cggtttcctt atttgtgtta tcggaatgga 120  
 ggaggagcgt ttttgattcc gtatttcctt acgttaatca tatgcggcat acctcttgct 180

```

tatctggaaa caacgcttgg acaattcgct agcgctgggt gcatatcggt cttcaatatt 240
aaccctttat tcaaagggtgc aggatacgcc gttatagttc taaatgtaat agcttcgata 300
tacttctcgg cgattatgtc atatccaata ctttacatat atcattcgat gagttcacca 360
ttaccttggc aaagttgtgg caattcctgg aacactgtga actgcaccga aataacagga 420
aactcgagtt ttttcacatc aaacggatct atcactacgc cggaagacga atacttccac 480
cgacacctct tgcaagtctc cccgaatatc aaccatatcg gaagtatagt tgctccagt 540
ttctggtgca acctgatttg ttggattctt gtgtatctgt gcatctgtaa cggggtcaag 600
agcgctcgaa agatcgata cttcacgta ttgtttcctt atgtggtctt gtccgtttta 660
ttcgtacgag ggataaccct ccctggcgct tggaagggca tcatgtttta tattcttccc 720
gattgggcac agctagctaa accgaaagta tgggcagatg cagcaacaca aatctttttc 780
tctcttggtc cgggctgggg tggctctcgc agcatgtcca gtttcaacaa atttcactac 840
aacaacttac ggtcatccat gattattcca atagtgaata gtgcaacaag catctgggag 900
ggttttgttg tattctcagt gctaggattt gctgctgaac gtactaatgt gccagttagc 960
caagtggcga ccgctgggtc tgggttagca ttgtttacgt acccggtac ggtgacgatg 1020
atgccagctc ctaatttgtg ggcaatcaca ttctttgtaa tgctgtttt ccttgggaata 1080
gatactatgt tcgtcactat cgaagctata atcgctggat tattggatga gtttcctaga 1140
ttcaaatac gtaaacgaat aatagctttc atcacctgcg tcgttcttt tagtttttct 1200
attatctgca atactgaggg agggctacat gtgattggat tactagactc ccatgtagcc 1260
atactttgtg tgccgctagt atgcgcgttg gagatcatag cagctgtcta cacatacgaa 1320
aacttcagtt tcgacgtact gttcatgacc ggccgacct tgagacgaat ctggatggta 1380
ttgtggagat atgttattct tttaataatta ttggtgatca cactgtatag tcttctggaa 1440
gtgtogagtt tagccggctg gttcattact cctgtttccg ttgtctgcat accgatttac 1500
gcagctaaaag ttttactacg ggcagaagga agtctgttgg agcgaatacg tgctagctgc 1560
cgtcctagca acgattgggg tccatcggag ccagaaaaaa gaagggaatg ggagttgctt 1620
aaaaaacaga aagctgatat ttttcggtg aatgatttag acaagtatta a 1671

```

<210> 6

<211> 556

<212> PRT

<213> Manduca sexta

<220>

<223> proline transporter

<400> 6

```

Met Ser Gly Ala Thr Gln Asp Arg Trp Gly Ser Gln Leu Glu Tyr Leu
  1              5              10              15

```

```

Leu Ser Cys Leu Gly Tyr Ala Val Gly Ile Gly Asn Leu Trp Arg Phe
          20              25              30

```

```

Pro Tyr Leu Cys Tyr Arg Asn Gly Gly Gly Ala Phe Leu Ile Pro Tyr
      35              40              45

```

```

Phe Leu Thr Leu Ile Ile Cys Gly Ile Pro Leu Val Tyr Leu Glu Thr
      50              55              60

```

```

Thr Leu Gly Gln Phe Ala Ser Ala Gly Cys Ile Ser Val Phe Asn Ile
      65              70              75              80

```

```

Asn Pro Leu Phe Lys Gly Ala Gly Tyr Ala Val Ile Val Leu Asn Val
          85              90              95

```

```

Ile Ala Ser Ile Tyr Phe Ser Ala Ile Met Ser Tyr Pro Ile Leu Tyr
      100             105             110

```

```

Ile Tyr His Ser Met Ser Ser Pro Leu Pro Trp Gln Ser Cys Gly Asn
      115             120             125

```



Ser	Trp	Asn	Thr	Val	Asn	Cys	Thr	Glu	Ile	Thr	Gly	Asn	Ser	Ser	Phe	
130						135					140					
Phe	Thr	Ser	Asn	Gly	Ser	Ile	Thr	Thr	Pro	Glu	Asp	Glu	Tyr	Phe	His	
145					150					155					160	
Arg	His	Leu	Leu	Gln	Val	Ser	Pro	Asn	Ile	Asn	His	Ile	Gly	Ser	Ile	
				165					170					175		
Val	Ala	Pro	Val	Phe	Trp	Cys	Asn	Leu	Ile	Cys	Trp	Ile	Leu	Val	Tyr	
			180					185					190			
Leu	Cys	Ile	Cys	Asn	Gly	Val	Lys	Ser	Val	Gly	Lys	Ile	Val	Tyr	Phe	
	195						200					205				
Thr	Val	Leu	Phe	Pro	Tyr	Val	Val	Leu	Ser	Val	Leu	Phe	Val	Arg	Gly	
	210					215					220					
Ile	Thr	Leu	Pro	Gly	Ala	Trp	Lys	Gly	Ile	Met	Phe	Tyr	Ile	Leu	Pro	
225					230					235					240	
Asp	Trp	Ala	Gln	Leu	Ala	Lys	Pro	Lys	Val	Trp	Ala	Asp	Ala	Ala	Thr	
			245						250					255		
Gln	Ile	Phe	Phe	Ser	Leu	Gly	Pro	Gly	Trp	Gly	Gly	Leu	Val	Ser	Met	
		260						265					270			
Ser	Ser	Phe	Asn	Lys	Phe	His	Tyr	Asn	Asn	Leu	Arg	Ser	Ser	Met	Ile	
		275					280					285				
Ile	Pro	Ile	Val	Asn	Ser	Ala	Thr	Ser	Ile	Trp	Ala	Gly	Phe	Val	Val	
	290					295					300					
Phe	Ser	Val	Leu	Gly	Phe	Ala	Ala	Glu	Arg	Thr	Asn	Val	Pro	Val	Ser	
305					310					315					320	
Gln	Val	Ala	Thr	Ala	Gly	Pro	Gly	Leu	Ala	Phe	Val	Thr	Tyr	Pro	Ala	
				325					330					335		
Thr	Val	Thr	Met	Met	Pro	Ala	Pro	Asn	Leu	Trp	Ala	Ile	Thr	Phe	Phe	
			340					345					350			
Val	Met	Leu	Phe	Phe	Leu	Gly	Ile	Asp	Thr	Met	Phe	Val	Thr	Ile	Glu	
	355						360					365				
Ala	Ile	Ile	Ala	Gly	Leu	Leu	Asp	Glu	Phe	Pro	Arg	Phe	Lys	Ser	Arg	
	370					375					380					
Lys	Arg	Ile	Ile	Ala	Phe	Ile	Thr	Cys	Val	Val	Leu	Phe	Ser	Phe	Ser	
385					390					395					400	
Ile	Ile	Cys	Asn	Thr	Glu	Gly	Gly	Leu	His	Val	Ile	Gly	Leu	Leu	Asp	
			405						410					415		
Ser	His	Val	Ala	Ile	Leu	Cys	Val	Pro	Leu	Val	Cys	Ala	Leu	Glu	Ile	
			420					425					430			
Ile	Ala	Ala	Val	Tyr	Thr	Tyr	Glu	Asn	Phe	Ser	Phe	Asp	Val	Leu	Phe	
	435						440					445				

Met Thr Gly Arg Pro Leu Arg Arg Ile Trp Met Val Leu Trp Arg Tyr  
450 455 460

Val Ile Leu Leu Ile Leu Leu Val Ile Thr Leu Tyr Ser Leu Leu Glu  
465 470 475 480

Val Ser Ser Leu Ala Gly Trp Phe Ile Thr Leu Val Ser Val Val Cys  
485 490 495

Ile Pro Ile Tyr Ala Ala Lys Val Leu Leu Arg Ala Glu Gly Ser Leu  
500 505 510

Leu Glu Arg Ile Arg Ala Ser Cys Arg Pro Ser Asn Asp Trp Gly Pro  
515 520 525

Ser Glu Pro Glu Lys Arg Arg Glu Trp Glu Leu Leu Lys Lys Gln Lys  
530 535 540

Ala Asp Ile Phe Pro Leu Asn Asp Leu Asp Lys Tyr  
545 550 555

<210> 7  
<211> 1995  
<212> DNA  
<213> Aedes aegypti

<220>  
<223> glutamate transporter

<400> 7  
tttcaaactg ggttgaaact gttgcactaa tcgctcttca aatgctgcta caatagcaat 60  
gatcgtgaaa cagtttcaaa cgtggttgaa tcggtttttt ttttttcggt ttgagaattt 120  
aaatcttgtc gagatagaaa tctttgttca tgatgaattt acagtagcac agagttttta 180  
acagcaaaat gtattagaga tatttgatga atcacaaaaa taaccgttcg tggattataa 240  
tagtaatgcg taatttgatg agagacccaa aacgacacag cgcatttcga cggcttatcc 300  
gtgcttctga gccattagc agcacgctga taagatgagg cgggagcagt tgcaagcctt 360  
cgtcaaggag aacctgctga cgtttttgac tatcggtgga gtcacgttg gcatagtgct 420  
tggaattggt ctccaggaag tgcccgcgga aggtgaaaaa tggacggcaa gagatgtagc 480  
ctacatcaac tttgtaggag atatcttctt cggatgctg aaagcactga tcctgcctct 540  
gattgttaca tcgctcatcg ctgctgtcgg ttcccttgat ctgctgcttt cgggaaaaat 600  
cggagggtcga gctgtcctgt actacgtgat aacaacggta atggcagtta ttttggaat 660  
tgtactcgtc gtaaccattc aaccgggcaa aggagccgaa gagacaagt gcgctgtaaa 720  
aggggaagta cgaacgtta caacggctga cactttgctg gacttggtac gaaacatgtt 780  
tccaccgaac ctggtccaag cttgcctaca gcaatatcaa actgttctga cacctcccaa 840  
aagtaacccg gtggaaacag atctgatcct ttggtctgtt ggtggtaaat ttgtcgatgg 900  
aatgaatatc attggtctgg tgggtggcatc gattgtattc ggaatagcac ttggagcact 960  
gaaagaagat gtccaactag tactgaagtt ctttcaacag ttgtcacata ccatcatgaa 1020  
agttacagga tgggttatat ggttgctgcc catcggagtg ttgtttttga ttactgcaa 1080  
actgttgga atggaagatc taggagccgt cttcggtaaa ctaggctctat actttgccgt 1140  
agttgctggt ggaattgtat tccacggatt cgtcattctt ccgctgttgt tcttctgtt 1200  
cactcgtaaa aatccagtca aatttgtagc aaacatgggt caagcgattg ccaccgcctt 1260  
cggaacctcg tcaagttcgg cgaccttgcc agtgactatg caatgcctcg aagacaaaaa 1320  
tcacatcgat ccacgtgtgt cccgatttgt gctaccgatt ggtgccacta tcaatatgga 1380  
cggcactgcc ttgtacgaag ctgtggccgc cattttcatt gctcaactca gaggactttc 1440  
gctcacattt gggaaacatag ttgccataag cataacagcg acagcagcca gcataggcgc 1500  
agcaggaatt cctcaggccg gattagtcac attggtcatg gtgctggata cagttggtct 1560  
accagcagaa gacgtatcac tcataatagc cgtggattgg tctgcccatt ttgttgatc gcttccgcac 1620  
cgtggtaaac gtgctgggag atagctttgg tgcggccatt gtcgcccact acagtcaaaa 1680  
ggaactgaca acaattccat ccagtgagat taacgggaaa actcaacgaa attctctggt 1740  
gcacagtgtc gagacagtgg tattcgaaga gaggctgtaa gcgaaactga tgaccacttt 1800

ttgattttaag catgttaata actcgtactg agtagatgac tcgatcttaa cgtaaaaact 1860  
aaggcaacca tgtcaaagta aagtgttatg ttattgaaaa attaaccgta ttaacttatg 1920  
atgtaaggta actgcaaaca ttgatattga atgaaataaa cgttatcctc aacaacaaga 1980  
aaaaaaaaaa aaaaa 1995

<210> 8  
<211> 481  
<212> PRT  
<213> Aedes aegypti

<220>  
<223> glutamate transporter

<400> 8  
Met Arg Arg Glu Gln Leu Gln Ala Phe Val Lys Glu Asn Leu Leu Thr  
1 5 10 15  
Phe Leu Thr Ile Gly Gly Val Ile Val Gly Ile Val Leu Gly Ile Gly  
20 25 30  
Leu Arg Glu Val Pro Ala Glu Gly Glu Lys Trp Thr Ala Arg Asp Val  
35 40 45  
Ala Tyr Ile Asn Phe Val Gly Asp Ile Phe Leu Arg Met Leu Lys Ala  
50 55 60  
Leu Ile Leu Pro Leu Ile Val Thr Ser Leu Ile Ala Ala Val Gly Ser  
65 70 75 80  
Leu Asp Leu Ser Leu Ser Gly Lys Ile Gly Gly Arg Ala Val Leu Tyr  
85 90 95  
Tyr Val Ile Thr Thr Val Met Ala Val Ile Leu Gly Ile Val Leu Val  
100 105 110  
Val Thr Ile Gln Pro Gly Lys Gly Ala Glu Glu Thr Ser Gly Ala Val  
115 120 125  
Lys Gly Glu Val Arg Asn Val Thr Thr Ala Asp Thr Leu Leu Asp Leu  
130 135 140  
Val Arg Asn Met Phe Pro Pro Asn Leu Val Gln Ala Cys Leu Gln Gln  
145 150 155 160  
Tyr Gln Thr Val Leu Thr Pro Pro Lys Ser Asn Pro Val Glu Thr Asp  
165 170 175  
Leu Ile Leu Trp Ser Val Gly Gly Lys Phe Val Asp Gly Met Asn Ile  
180 185 190  
Ile Gly Leu Val Val Ala Ser Ile Val Phe Gly Ile Ala Leu Gly Ala  
195 200 205  
Leu Lys Glu Asp Val Gln Leu Val Leu Lys Phe Phe Gln Gln Leu Ser  
210 215 220  
His Thr Ile Met Lys Val Thr Gly Trp Val Ile Trp Leu Ser Pro Ile  
225 230 235 240



caatccacgt	ggaacaacat	gacgacgaac	aggacaaaaga	gaactccaag	ttactctcgg	240
cgcactcacc	ggcaccacgc	ataaccccat	cggggcaaat	gcgaaaagta	aagagtttca	300
gtgatacaca	caagatacga	gatgtgacca	ctgcttcagg	cgcagcgtcg	gcgcggagtc	360
tgcgtcccta	cgaaatagtg	aacacgtatc	ccgagggatc	agaaagtggg	actaacaatt	420
atggagcacc	gtccgtccgg	tcgcttgctt	ccatcggaat	gggttgtagc	gacggacgta	480
aaatggttat	tagacgagta	ccaacatcgc	ccacggaatt	gttccatcta	gttcgtcctc	540
ctacgcctcc	cgacgaagat	tcggcgctcg	acgaaagtga	ttgcgaggaa	gaagaagaag	600
atgctgcggt	tcacctcaag	ccacgcaggc	ccttctgggc	caacaagata	cagttcgtgc	660
tggcttgctg	gggatattcc	gtcggcctcg	gcaacgtgtg	gcgcttccct	tatctctgct	720
acaaaagtgg	aggaggggca	ttcctcattc	catacttcac	cattctatta	atttgcgggc	780
tgccaatgct	cttcatggaa	ctcgccatag	gacagtatac	agcacacggc	cctattgggg	840
ctctatcaca	aatttgtcca	ctttttaaag	gcgctgggct	agcaagtgtg	gtgatctcat	900
ttctaattgc	cacgtattac	gctgtgataa	ttgcatgggc	catatattat	tttttcacat	960
cattcaaaac	cgaagtacct	tgggcaagtt	gctccaatcg	atggaacaca	gaccaatgct	1020
gggttccaaa	tcacaacccat	acgaaaccga	acggatcaca	aacacccacc	gaacaatttt	1080
tcgagagaaa	ggtattgaat	atgagtgtcg	gtattgagta	tcctgggtggc	atgcggtggg	1140
aattggcagc	ttgcttggtc	tgtgcttggg	tgtagtttta	tttcgcccta	tggaaaagca	1200
ttaaatcttc	agccaaagtt	cgttatatca	caacaacact	gccatttctg	ctgattatag	1260
tctttcttgg	acggctctttg	acactcgatg	gagcagatgg	aggcttgagg	ttcttcttta	1320
aaccagactg	ggaacttttta	aaacagtcca	ggccttgggt	caacgctgcg	tcacagatct	1380
ttactctat	cggaatagca	ttcgggtcga	tgatcatggt	cgttctttac	aaccgattcg	1440
acaacaactt	cctgcacgat	accgtagccg	tcactctagt	caacgctatt	actagtctca	1500
tagttggcat	attcaccttt	gctaccatcg	gaaatatcgc	cttcgaacaa	aatactcccg	1560
tgaaggatgt	catagccgac	agtccaggcc	tattatttgt	agtgtaccgg	caagctatag	1620
caaaaatgcc	agcatctcag	ctatgggcag	tactgttctt	cttcatgttt	ctatgccttg	1680
gattaaatag	tcaatttgct	atagtggaa	tggtcgtgac	ttcaatacaa	gacggatttc	1740
ccgacatgat	acgaaaaaga	cttgtgtatc	atgaattatt	agtactgctt	gtgtgtgcgg	1800
tgtcattatt	atgcggactg	ccacacatta	ttcatagcgg	tatatatgta	ttccagttaa	1860
tggattatta	cgcgcgctcg	ctcagtataa	cttatctcgc	cttttttgag	gtggtcgcga	1920
ttgcatggtt	ttatggcggtg	ggaagactgt	ctagaaatat	taaacaaatg	acaggtcgcc	1980
aaccatcgct	atactttcga	ttctgttggc	tgcagcgtc	accggcgctg	ctgttagcgt	2040
tgtgggtggc	aagcatggtc	gactacacgc	cgctagtta	caggcagtac	caatatcccg	2100
catgggcaca	agctctcgga	tggatcatgg	cttccctctc	cttactttgc	atcccagtat	2160
acgcggttat	agttataatt	agagcacctg	gagacagttt	aagagagaaa	ctacgttact	2220
caatacaacc	aacatctata	tgtgaatgtg	gtgtaaatgg	ctgtgacatc	tgctgctctg	2280
agtcggatcc	gccggacgac	aaaacagtta	ttaatagta	taatgaaacc	gtatatttta	2340
aagagtatta	ttaaaaatga	taagaattaa	gtactccctc	tgccacgagg	aacaaataac	2400
atttgggcct	gcgttcttta	tgacgatata	gattcaacac	ggtatgtttg	taacgaataa	2460
tcaagtttaa	taaggacata	taaaattaa	taactggcat	ataccagaaa	atctatttag	2520
tcatactgaa	tcocatgtta	gggcgctgac	caatttctta	tcgatttttt	gattcgcacc	2580
tgtgtaactg	acaaagtttg	tcatcgaaaa	ttaccgtcta	gaagaggtag	tcgtgataaa	2640
caatactacg	tagataattt	acaacgatct	tccatcataa	gtacacatca	ctcgacctcg	2700
acctacaatt	atgagcattc	accaaacagt	gtcatgacat	acataactat	ggtcatataa	2760
attttatata	gttacaatgt	aggagtgaag	atcatgtatg	tacttctgac	gtcgcgcgat	2820
aatgcattga	cttcgatagt	ataaatagca	tttaaatcat	atcattacaa	agaaatacac	2880
ctattgttat	atattttttac	tatgcacata	ttaaaaacta	tgtgttagcg	gtaactgtgt	2940
tctgtgtagg	tattcataat	agcagaaatg	tattattact	gaatgtttgt	aaagctttat	3000
attctcccag	tcacgatatt	atattgcata	agtatgtaaa	tatgtaattt	aaggcccgac	3060
caccagcaaa	ccagagctta	acagattctt	agaagccatt	tatccaaatt	tataacatac	3120
taaaaaaaat	atttaaataa	tttaagaaat	atttaaaaga	catatttttg	caatgtgtta	3180
tctttatttt	aattgtataa	aattttttata	atagaatatt	gtttcggtta	tttcattgtg	3240
aaaatgcaat	taaaattggt	gactccgtgc	attttctcat	aaacatgaat	caagtactct	3300
aacactatta	gaaagacaat	tttataaaga	atatttttgt	agttcctatt	taaatttttt	3360
tttttgaatg	aactatcgta	aatctttgca	atttggcgcc	ggtaacctgc	gcgctgccaa	3420
gttccatata	aacgaatcgc	tcaaggacgt	ttgctagggg	agggacctta	cataatgggtc	3480
tgttttatag	gctggtctac	aacctagtaa	tacctatgta	gtgttgaaac	accgaataaa	3540
ttattttta	cgttgtggaa	atttgtgtag	atccttaccg	ataaagattt	caaaataact	3600
tcccggtaaa	attatgtagg	tatacagtga	aatttgatta	aagtgagcct	tggacaatat	3660
atgagaaacc	actgctaata	ataattgcaa	taaggctccg	gtacttttgc	attaagcctc	3720
ttttactggg	aatttcaaac	ctcgtttaatt	gagaatcgat	ttcttagatt	ttacgatgtt	3780
catctctata	attgagactt	ggtaggtcaa	tcacctatat	cagtaaaaca	atttatcagg	3840

```

tttggttaagg ttacgactcg tttgtataca aatatttttaa ttactttctgc acatttttttaa 3900
ccactcttgt catctatctc tataaataag acaactgtca ttgcaaacct ccctatttgt 3960
atactggcta aataaaaaatg ctctatacaa atcctaactc ctttgagatc ccagttaaat 4020
agttgtatag atttcactgt attatacatt tctagccatt tttatgtcaa tgttcatgtt 4080
attgaataat cggcgataaa catcctcaaa tcgtaggaca taaataagct atacgattta 4140
catatacact agtaatatgt agcaacaaca taaacctttg agggcatcag tattaatttt 4200
taagttaagt atcaggcctt ttatattatt ttatttttctt aaaaggataa atattttaatc 4260
atatttgtaa ccatcgaccg tacttgcata ggtatataat atatatattgt tgtgttgtaa 4320
gattgttttt cctgaataat gtgaccgaaa acattccata aatacctata ctcatgtaat 4380
ttaaagatag ttttaatat tttagatagt tattttatttt gcatacctta taaaacatgg 4440
atgttaagaa tatgtaagca aattgtatta cttaagtaac tatctcagta aataggtagg 4500
ttgccacaga aattgtaatt tttcgtcaat cactaaaata aaatgactgc ttagccgtga 4560
gcatagccgg ggggggcaac gttaggcggc acccacccta taagccctgc gttacctctg 4620
taacgatgtc tctacatcgc gtgatacagg ctttttttaa atcagcgggt tttttcctcg 4680
ccagcgggtc cttcctagat aaaatccgta gctacgccaa ccttccgagt actaaacaaa 4740
acatgaaaca atattatttg ttgttatctg ccactgatat agaattctac atacctacgt 4800
aaaatcagtc ttttgaaaag taaatcgttc ataattatta tagtgtaaat aggtacattt 4860
tttgtatata agtaaaataa gtaacggcaa ggtatcataa ggcaaaaagcg aaataaagtc 4920
ctaagggtta tgagcaaaaa aaaaaaaaaa aaaaaa 4956

```

<210> 10

<211> 727

<212> PRT

<213> Manduca sexta

<220>

<223> neurotransmitter transporter encoded by inebriated  
gene

<400> 10

```

Met Asn Lys Val Glu Ser Ser Thr Glu Ala Ala Ala Pro Ser Val Ala
  1                      5                      10                      15

```

```

Ile His Val Glu Gln His Asp Asp Glu Gln Asp Lys Glu Asn Ser Lys
      20                      25                      30

```

```

Leu Leu Ser Ala His Ser Pro Ala Pro Ser Ile Thr Pro Ser Gly Gln
      35                      40                      45

```

```

Met Arg Lys Val Lys Ser Phe Ser Asp Thr His Lys Ile Arg Asp Val
      50                      55                      60

```

```

Thr Thr Ala Ser Gly Ala Ala Ser Ala Arg Ser Leu Arg Pro Tyr Glu
      65                      70                      75                      80

```

```

Ile Val Asn Thr Tyr Pro Glu Gly Ser Glu Ser Gly Thr Asn Asn Tyr
      85                      90                      95

```

```

Gly Ala Pro Ser Val Arg Ser Leu Ala Ser Ile Gly Met Gly Cys Thr
      100                      105                      110

```

```

Asp Gly Arg Lys Met Val Ile Arg Arg Val Pro Thr Ser Pro Thr Glu
      115                      120                      125

```

```

Leu Phe His Leu Val Arg Pro Pro Thr Pro Pro Asp Glu Asp Ser Ala
      130                      135                      140

```

```

Ser His Glu Ser Asp Cys Glu Glu Glu Glu Glu Asp Ala Ala Val His
      145                      150                      155                      160

```

Leu Lys Pro Arg Arg Pro Phe Trp Ala Asn Lys Ile Gln Phe Val Leu  
 165 170 175  
 Ala Cys Val Gly Tyr Ser Val Gly Leu Gly Asn Val Trp Arg Phe Pro  
 180 185 190  
 Tyr Leu Cys Tyr Lys Ser Gly Gly Gly Ala Phe Leu Ile Pro Tyr Phe  
 195 200 205  
 Ile Ile Leu Leu Ile Cys Gly Val Pro Met Leu Phe Met Glu Leu Ala  
 210 215 220  
 Ile Gly Gln Tyr Thr Ala His Gly Pro Ile Gly Ala Leu Ser Gln Ile  
 225 230 235 240  
 Cys Pro Leu Phe Lys Gly Ala Gly Leu Ala Ser Val Val Ile Ser Phe  
 245 250 255  
 Leu Met Ser Thr Tyr Tyr Ala Val Ile Ile Ala Trp Ala Ile Tyr Tyr  
 260 265 270  
 Phe Phe Thr Ser Phe Lys Thr Glu Val Pro Trp Ala Ser Cys Ser Asn  
 275 280 285  
 Arg Trp Asn Thr Asp Gln Cys Trp Val Pro Asn His Asn His Thr Lys  
 290 295 300  
 Pro Asn Gly Ser Gln Thr Pro Thr Glu Gln Phe Phe Glu Arg Lys Val  
 305 310 315 320  
 Leu Asn Met Ser Ala Gly Ile Glu Tyr Pro Gly Gly Met Arg Trp Glu  
 325 330 335  
 Leu Ala Ala Cys Leu Val Cys Ala Trp Val Leu Val Tyr Phe Ala Leu  
 340 345 350  
 Trp Lys Ser Ile Lys Ser Ser Ala Lys Val Arg Tyr Ile Thr Thr Thr  
 355 360 365  
 Leu Pro Phe Leu Leu Ile Ile Val Phe Leu Gly Arg Ser Leu Thr Leu  
 370 375 380  
 Asp Gly Ala Asp Gly Gly Leu Arg Phe Phe Phe Lys Pro Asp Trp Glu  
 385 390 395 400  
 Leu Leu Lys Gln Ser Arg Pro Trp Val Asn Ala Ala Ser Gln Ile Phe  
 405 410 415  
 Asn Ser Ile Gly Ile Ala Phe Gly Ser Met Ile Met Phe Ala Ser Tyr  
 420 425 430  
 Asn Arg Phe Asp Asn Asn Phe Leu His Asp Thr Val Ala Val Thr Leu  
 435 440 445  
 Val Asn Ala Ile Thr Ser Leu Ile Val Gly Ile Phe Thr Phe Ala Thr  
 450 455 460  
 Ile Gly Asn Ile Ala Phe Glu Gln Asn Thr Pro Val Lys Asp Val Ile  
 465 470 475 480

Ala Asp Ser Pro Gly Leu Leu Phe Val Val Tyr Pro Gln Ala Ile Ala  
 485 490 495  
 Lys Met Pro Ala Ser Gln Leu Trp Ala Val Leu Phe Phe Phe Met Phe  
 500 505 510  
 Leu Cys Leu Gly Leu Asn Ser Gln Phe Ala Ile Val Glu Val Val Val  
 515 520 525  
 Thr Ser Ile Gln Asp Gly Phe Pro Asp Met Ile Arg Lys Arg Leu Val  
 530 535 540  
 Tyr His Glu Leu Leu Val Leu Leu Val Cys Ala Val Ser Leu Leu Cys  
 545 550 555 560  
 Gly Leu Pro His Ile Ile His Ser Gly Ile Tyr Val Phe Gln Leu Met  
 565 570 575  
 Asp Tyr Tyr Ala Ala Ser Leu Ser Ile Thr Tyr Leu Ala Phe Phe Glu  
 580 585 590  
 Val Val Ala Ile Ala Trp Phe Tyr Gly Val Gly Arg Leu Ser Arg Asn  
 595 600 605  
 Ile Lys Gln Met Thr Gly Arg Gln Pro Ser Leu Tyr Phe Arg Phe Cys  
 610 615 620  
 Trp Leu Ile Ala Ser Pro Ala Leu Leu Leu Ala Leu Trp Val Ala Ser  
 625 630 635 640  
 Met Val Asp Tyr Thr Pro Pro Ser Tyr Arg Gln Tyr Gln Tyr Pro Ala  
 645 650 655  
 Trp Ala Gln Ala Leu Gly Trp Ile Met Ala Ser Leu Ser Leu Leu Cys  
 660 665 670  
 Ile Pro Val Tyr Ala Val Ile Val Ile Ile Arg Ala Pro Gly Asp Ser  
 675 680 685  
 Leu Arg Glu Lys Leu Arg Tyr Ser Ile Gln Pro Thr Ser Ile Cys Glu  
 690 695 700  
 Cys Gly Val Asn Gly Cys Asp Ile Cys Cys Ser Glu Ser Asp Pro Pro  
 705 710 715 720  
 Asp Asp Lys Thr Val Ile Asn  
 725

<210> 11  
 <211> 2034  
 <212> DNA  
 <213> Manduca sexta

<220>  
 <223> orphan transporter

<400> 11  
 atggcgggcca aagctgagcc tattggaccc cgtaatggac acgagttggc gccgttgacc 60  
 actcgttctg atggctctga aaggcctcat ggtgttacta tcgttcttca aggatcacga 120  
 gggctccttg aacgtgatgc tcctgaggaa gaccgcgctg cgtggtcagg gaagctccag 180



```

tttttccctgt ccatcattgg gtattcgggtc ggcctgggca atatatggcg attccccgtat 240
ttgtgtcaac aaaatggcgg cggtgccttc ctaatcccgt tectcatcat gttggtgctg 300
gaaggcatcc cgctcttccat gatcgagatg gccatcgggt agaagatgcg cctgggctcc 360
ctcggagtgt ggaacacccat ccacccatgg ctcggcggca tcggcatctc cagttgctg 420
gtgacactct tcgtggctct ttactataac gtgatcatca cttgggtgtt tttctatctc 480
ttcaatagta tacggttaac agccgatcaa ctaccatggg ctcatgccc ttacgacaac 540
ggtacagccg aggtggaatg caacaaggcc tctgccacgg tctacttctg gtaccgag 600
gccctggatg cctccccag catcgatgag cggggcgtgc cgcggtggtg gatagtactc 660
tacctcctgc tggcttgat catcgtgttc ttcattgtga tgaaggggat ccagagtagt 720
gggaagggtg tttacttcac atctctgttc ccttacgagg tctgacgat cttcttcgtg 780
cgcggcatca cgttgcccgg ctcttcggat gggatcctgc acatgtataa acctaagctg 840
gagaaacttc tagacccaac ggtgtgtggc tggacgcggc ttacacaagt gttctactcc 900
ttcgggctcg cgttcggctc cctcatcgcc ttcggctcct ataaccctcc gaacaataac 960
tgcgtgaggg atgtcctcct ggtctccgtg tgtaacgccc taacagcgat ctacgcgtcc 1020
gtggtcatct tcagcatcct cggcttcaag gcttatacca tgggtggagaa ctgtattgtc 1080
aaggagatta aagtcctagc cctgcatcat atcgggggct tcacgctcaa ctccacggca 1140
gattactatc gggagcagtt cccgagactg aacgggtacgg ccatagcagc cctcaacctc 1200
actggatgca ccatgagtcg gcagcttgag gaggcagctg aaggcacggg gctagctttc 1260
atagtgttca cgcaggctat tctgaagctt acaccagctc ctttctgggt catcatattc 1320
ttctcatgct tgctgtctct gggccttgga agccagatcg gcatcatgga aggaatgctg 1380
tgcaccatct ttgatatcga cttcttcaag aggttgagca agccagttat cactggcgtg 1440
gtctgacctt tctgtttctt cgtggggctc atcttcacga ccggcgcggg agagtactgg 1500
ttgaagatgt tcgactcgtt cgccggcact attggtctcg tcgtcgtcgc tctgctaaag 1560
atgatcgctg ttatttcat ctatggacat gagaagttaa caaacgacat ctacgagatg 1620
actggctacc gccccggcat ctactggcaa gtgacgtggc gctacgtggg ccccgccatc 1680
gtcacctgca tctgtctctc gtccctcgtg ttcattgctc tcaaccgcc catgtacggc 1740
gcttggaatg ctgacgaggg tcgctgcatt aagacaccct acccaacctg ggtgttggtg 1800
atcgctgtct tgatgatcct ggctggcgtg ctgccaattc cagtggtttt gctgctgcga 1860
aggttccagt gtctcgctt cgacgttgac atccaccagg gctccatcag gaggattgag 1920
accacgtct cactaagga gatgatgagt gatcaggata acgtggagag cagcgaggag 1980
cgccccaaaca agcgcctgcc cgccggcatc gcgcgcagtc gccccaaaga ataa 2034

```

<210> 12  
 <211> 676  
 <212> PRT  
 <213> Manduca sexta

<220>  
 <223> orphan transporter

```

<400> 12
Met Ala Ala Lys Ala Glu Pro Ile Gly Pro Arg Asn Gly His Glu Leu
  1              5              10              15

Ala Pro Leu Thr Thr Arg Ser Asp Gly Ser Glu Arg Pro His Gly Val
      20              25              30

Thr Ile Val Leu Gln Gly Ser Arg Gly Ser Leu Gln Arg Asp Ala Pro
  35              40              45

Glu Glu Asp Arg Ala Ala Trp Ser Gly Lys Leu Gln Phe Phe Leu Ser
  50              55              60

Ile Ile Gly Tyr Ser Val Gly Leu Gly Asn Ile Trp Arg Phe Pro Tyr
  65              70              75              80

Leu Cys Gln Gln Asn Gly Gly Gly Ala Phe Leu Ile Pro Phe Leu Ile
      85              90              95

```

Met	Leu	Val	Leu	Glu	Gly	Ile	Pro	Leu	Val	Leu	Ile	Glu	Met	Ala	Ile		
			100					105					110				
Gly	Gln	Lys	Met	Arg	Leu	Gly	Ser	Leu	Gly	Val	Trp	Asn	Thr	Ile	His		
		115					120					125					
Pro	Trp	Leu	Gly	Gly	Ile	Gly	Ile	Ser	Ser	Cys	Val	Val	Thr	Leu	Phe		
	130					135					140						
Val	Ala	Leu	Tyr	Tyr	Asn	Val	Ile	Ile	Thr	Trp	Val	Phe	Phe	Tyr	Leu		
145					150					155					160		
Phe	Asn	Ser	Ile	Arg	Leu	Thr	Ala	Asp	Gln	Leu	Pro	Trp	Ala	His	Cys		
				165					170					175			
Pro	Tyr	Asp	Asn	Gly	Thr	Ala	Glu	Ala	Glu	Cys	Asn	Lys	Ala	Ser	Ala		
			180					185					190				
Thr	Val	Tyr	Phe	Trp	Tyr	Arg	Glu	Ala	Leu	Asp	Ala	Ser	Pro	Ser	Ile		
	195						200					205					
Asp	Glu	Pro	Gly	Val	Pro	Arg	Trp	Trp	Ile	Val	Leu	Tyr	Leu	Leu	Leu		
210						215					220						
Ala	Trp	Ile	Ile	Val	Phe	Phe	Ile	Val	Met	Lys	Gly	Ile	Gln	Ser	Ser		
225					230					235					240		
Gly	Lys	Val	Val	Tyr	Phe	Thr	Ser	Leu	Phe	Pro	Tyr	Ala	Val	Leu	Thr		
				245					250					255			
Ile	Phe	Phe	Val	Arg	Gly	Ile	Thr	Leu	Pro	Gly	Ser	Ser	Asp	Gly	Ile		
			260					265					270				
Leu	His	Met	Tyr	Lys	Pro	Lys	Leu	Glu	Lys	Leu	Leu	Asp	Pro	Thr	Val		
		275					280					285					
Trp	Leu	Asp	Ala	Ala	Thr	Gln	Val	Phe	Tyr	Ser	Phe	Gly	Leu	Ala	Phe		
	290					295					300						
Gly	Ser	Leu	Ile	Ala	Phe	Gly	Ser	Tyr	Asn	Pro	Pro	Asn	Asn	Asn	Cys		
305					310					315					320		
Val	Arg	Asp	Val	Leu	Leu	Val	Ser	Val	Cys	Asn	Ala	Leu	Thr	Ala	Ile		
				325					330					335			
Tyr	Ala	Ser	Val	Val	Ile	Phe	Ser	Ile	Leu	Gly	Phe	Lys	Ala	Tyr	Thr		
			340					345					350				
Met	Val	Glu	Asn	Cys	Ile	Val	Lys	Glu	Ile	Lys	Val	Leu	Ala	Leu	His		
		355					360					365					
His	Ile	Gly	Gly	Phe	Thr	Leu	Asn	Ser	Thr	Ala	Asp	Tyr	Tyr	Arg	Glu		
	370					375					380						
Gln	Phe	Pro	Arg	Leu	Asn	Gly	Thr	Ala	Ile	Ala	Ala	Leu	Asn	Leu	Thr		
385					390					395					400		
Gly	Cys	Thr	Met	Ser	Arg	Gln	Leu	Glu	Glu	Ala	Ala	Glu	Gly	Thr	Gly		
				405					410					415			

Leu Ala Phe Ile Val Phe Thr Gln Ala Ile Leu Lys Leu Thr Pro Ala  
 420 425 430  
 Pro Phe Trp Ser Ile Ile Phe Phe Leu Met Leu Leu Ser Leu Gly Leu  
 435 440 445  
 Gly Ser Gln Ile Gly Ile Met Glu Gly Met Leu Cys Thr Ile Phe Asp  
 450 455 460  
 Ile Asp Phe Phe Lys Arg Leu Ser Lys Pro Val Ile Thr Gly Val Val  
 465 470 475 480  
 Cys Thr Phe Cys Phe Phe Val Gly Leu Ile Phe Thr Thr Gly Ala Gly  
 485 490 495  
 Glu Tyr Trp Leu Lys Met Phe Asp Ser Phe Ala Gly Thr Ile Gly Leu  
 500 505 510  
 Val Val Val Ala Leu Leu Lys Met Ile Ala Val Ile Tyr Ile Tyr Gly  
 515 520 525  
 His Glu Lys Phe Thr Asn Asp Ile Tyr Glu Met Thr Gly Tyr Arg Pro  
 530 535 540  
 Gly Ile Tyr Trp Gln Val Thr Trp Arg Tyr Val Gly Pro Ala Ile Val  
 545 550 555 560  
 Thr Cys Ile Leu Leu Ser Ser Leu Val Phe Met Leu Ile Asn Pro Pro  
 565 570 575  
 Met Tyr Gly Ala Trp Asn Ala Asp Glu Gly Arg Val Ile Lys Thr Pro  
 580 585 590  
 Tyr Pro Thr Trp Val Leu Val Ile Ala Val Leu Met Ile Leu Ala Gly  
 595 600 605  
 Val Leu Pro Ile Pro Val Val Leu Leu Leu Arg Arg Phe Gln Cys Leu  
 610 615 620  
 Ala Phe Asp Val Asp Ile His Gln Gly Ser Ile Arg Arg Ile Glu Thr  
 625 630 635 640  
 Thr Val Ser Thr Lys Glu Met Met Ser Asp Gln Asp Asn Val Glu Ser  
 645 650 655  
 Ser Glu Glu Arg Pro Asn Lys Arg Leu Pro Ala Gly Ile Ala Arg Ser  
 660 665 670  
 Arg Pro Lys Lys  
 675

<210> 13  
 <211> 3513  
 <212> DNA  
 <213> Manduca sexta  
  
 <220>  
 <223> GABA transporter

<400> 13

ccacgcgtcc	ggcgggtgcgc	ttgcgacaac	acctcctcgg	cgatattgtg	acggcttttcg	60
gtctgtgatg	tgttgtgttg	tggattgtga	tggtttttga	tattcaaaat	tagcaacggc	120
ccaatttcta	gtcaacgtac	ttcttttaaac	atggttggtac	attccaccta	agtcaaaaat	180
aaattgggat	agcgggtccag	tgtgctgaag	aaattttata	aaggtttcga	agagataaaa	240
cgagaaggag	acatggaaac	aaaaaatgat	tcacgaagcg	acgacatcga	acttagcgcg	300
caaggcagcg	gtaacaaacc	gagcgtatgtc	gcagtcaaat	caaatttacc	cgaaagaggc	360
tcctgggcca	gcaaactcga	cttcacccctc	tctgtcatcg	gcttggcgat	cggctcttggc	420
aatgtctggc	gttttctcta	cctctgctac	aagaacggtg	gtggtgcctt	cctcatccct	480
tacttcttga	ctctcttctt	cgctgggtatt	ccgatgttct	tcattggaact	cgctatggga	540
cagatgttga	ctatcggagg	acttgggtgtg	ttcaagatcg	ccccattttt	caaagggtatc	600
ggttatgctg	cagctgtcat	gtcctgctgg	atgaacgtgt	actacatagt	tatccttgct	660
tgggccatct	tctatttctt	catgtccatg	agatcagatg	tccctggag	gaactgcgac	720
aaatttttga	acacagccac	ttgcgtcaac	ccctacgata	ggaagaacct	tacatgctgg	780
tcctcgctgg	gcgatattgag	caccttctgc	accctgaacg	gaaggaatgt	tagcaaagct	840
gtcctctccg	accccggttaa	ggaattctgg	gaacgccgcg	ctcttcaa	ctcttctgga	900
attgaacaca	tcggcaacat	ccgctgggag	ctggcgggga	ctctgcttct	tgtctgggtt	960
ctgtgctact	tctgcatctg	gaagggtgtc	aggtggaccg	gcaaggctcg	ttacttcacc	1020
gccttggtcc	catacttctt	gtcactgtt	ctgctgatca	gaggaattac	cctccccgga	1080
gcatggaag	gcattaagtt	ctacgtaatg	cccaatatgt	cgaaactcct	ggagtctgaa	1140
gtgtggatcg	atgctgtcac	tcagatcttc	ttctcttatg	gccttgggtt	gggcacatc	1200
gtcgcttgg	gaagctacaa	caagttcac	aataattgtt	acaaagacgc	tttgattagtc	1260
tgtcgggtga	actccagtac	ttctatgttc	gtggtttctg	tgatcttctc	cgtggtcggg	1320
ttcatggcgc	atgagcagca	acggccagtt	gctgaggttg	ccgcatcagg	tcctggctta	1380
gccttccctg	cgtaaccatc	agcagttctc	caacttcccg	gcgctccact	ctggtcttgt	1440
ctcttcttct	tcattgctgt	gtcctcggg	ttggatagcc	agttctgcac	catggaagga	1500
ttcatcaccg	ccgtcattga	cgagtggccc	aaactcctca	gaaggaggaa	ggaaatcttc	1560
atcgccatta	cttgcattcat	ctcgtacctg	gtcggactgt	cttgatatatc	tgagggtggt	1620
atgtacgtgt	tccaaatcct	ggactcctac	gccgtgtctg	gcttctgtct	gctgttccctg	1680
atcttcttctg	agtgcgtgtc	catctcgtgg	gcgttcggcg	tgaatcgctt	ctacgacggt	1740
atcaaggaga	tgatcggcta	ctaccccacc	atttggtgga	agttctgctg	ggtcggcttc	1800
acgcctgcta	tttgtattag	cgtcttcac	ttcaacttgg	tgacgtggac	tccgatcaag	1860
tacatgaact	acgaatatcc	ctggtggtcc	cacgcttttg	gctggtttac	cgcgctgtcg	1920
tccatgctgt	gcattccctgg	atacatgatc	tacttgtgga	gagtcacgcc	tggcacttgg	1980
caagagaaat	tccacaaaat	cgtccgtatt	ccggaagatg	tgcttctctc	tcgaaccaag	2040
atgtaggccg	aagaacaggc	gaaacacgca	caaacacgca	caggcgtaga	cgcagccaac	2100
aacaatgcag	gtccaataac	ttacaagata	tttataacag	taagacagaa	ttttaagcc	2160
aatagaagat	atataggtaa	taaaataact	tacaattgtc	atgttctctc	tgtcattaag	2220
ccgccatatg	acagagagag	cgtgatatac	aaaagacgtt	ggacttgcaa	agttaacaca	2280
acgacttact	taacatcagg	atctcaggga	gttgagaatt	catttggaat	gggattcaga	2340
tgtgattatg	gtcttggttc	atttgcaaaa	tttaattttaa	aagttgttaa	ctacagacaa	2400
gcttttaaaac	tttttaataa	tcaatatgca	tcagtttact	ctcaattgtc	atcgatatatt	2460
atgaaaccat	ggaacaaaat	tataaggacg	tcagtaacgg	agtttgatat	tctaaatatt	2520
tacgcacaat	tagctatcat	gtgccaatat	cgcagtattt	ataatatatt	aacctcatgt	2580
tatatattaga	tccccgtcta	tataaaatcg	ggcaaagtag	tttatacaat	attacgggac	2640
gaatatttgt	ggagcgtatt	ttctattccc	aaatatcttt	cctggtccat	agtaggacat	2700
attcgtctac	gctagtctag	atctatgtat	gtgattttta	gaaaataata	atatttaggc	2760
ctaagataat	ttgatgactt	tccgtttgaa	cagtgtgtgc	gttgcgacgc	gtttacgtat	2820
gtttacattt	tacaattatt	tataaggttt	agatttttaag	tgaaaatata	ttttaattat	2880
tatctgtctt	ccattttaact	tagtgtttaag	gtttttgaat	ccacgcgtcc	ggcgggtgcgc	2940
ttgcgacaac	acctcctcgg	cgatattgtg	acggcttttcg	gtctgtgatg	tgttgtgttg	3000
tggattgtga	tggtttttga	tattcaaaat	tagcaacggc	ccaatttcta	gtcaacgtac	3060
ttcttttaaac	atgttggtac	attccaccta	agtcaaaaat	aaattgggat	agcgggtccag	3120
tgtgctgaag	aaattttata	aaggtttcga	agagataaaa	cgagaaggag	acatggaaac	3180
aaaaaatgat	tcacgaagcg	acgacatcga	acttagcgcg	caaggcagcg	gtaacaaacc	3240
gagcgtatgtc	gcagtcaa	caaatttacc	cgaaagaggc	tcctgggcca	gcaaactcga	3300
cttcacccctc	tctgtcatcg	gcttggcgat	cggctcttggc	aatgtctggc	gttttctcta	3360
cctctgctac	aagaacggtg	gtggtgcctt	ctcatccct	tacttcttga	ctctcttctt	3420
cgctgggtatt	ccgatgttct	tcattggaact	cgctatggga	cagatgttga	ctatcggagg	3480
acttggtgtg	ttcaagatcg	ccccattttt	caa			3513

<210> 14  
 <211> 597  
 <212> PRT  
 <213> Manduca sexta

<220>  
 <223> GABA transporter

<400> 14  
 Met Glu Thr Lys Asn Asp Ser Arg Ser Asp Asp Ile Glu Leu Ser Ala  
   1                  5                  10                  15  
 Gln Gly Ser Gly Asn Lys Pro Ser Asp Val Ala Val Lys Ser Asn Leu  
           20                  25                  30  
 Pro Glu Arg Gly Ser Trp Ala Ser Lys Leu Asp Phe Ile Leu Ser Val  
           35                  40                  45  
 Ile Gly Leu Ala Ile Gly Leu Gly Asn Val Trp Arg Phe Pro Tyr Leu  
       50                  55                  60  
 Cys Tyr Lys Asn Gly Gly Gly Ala Phe Leu Ile Pro Tyr Phe Leu Thr  
       65                  70                  75                  80  
 Leu Phe Leu Ala Gly Ile Pro Met Phe Phe Met Glu Leu Ala Met Gly  
           85                  90                  95  
 Gln Met Leu Thr Ile Gly Gly Leu Gly Val Phe Lys Ile Ala Pro Ile  
           100                  105                  110  
 Phe Lys Gly Ile Gly Tyr Ala Ala Ala Val Met Ser Cys Trp Met Asn  
       115                  120                  125  
 Val Tyr Tyr Ile Val Ile Leu Ala Trp Ala Ile Phe Tyr Phe Phe Met  
       130                  135                  140  
 Ser Met Arg Ser Asp Val Pro Trp Arg Asn Cys Asp Asn Tyr Trp Asn  
       145                  150                  155                  160  
 Thr Ala Thr Cys Val Asn Pro Tyr Asp Arg Lys Asn Leu Thr Cys Trp  
           165                  170                  175  
 Ser Ser Leu Gly Asp Met Ser Thr Phe Cys Thr Leu Asn Gly Arg Asn  
       180                  185                  190  
 Val Ser Lys Ala Val Leu Ser Asp Pro Val Lys Glu Phe Trp Glu Arg  
       195                  200                  205  
 Arg Ala Leu Gln Ile Ser Ser Gly Ile Glu His Ile Gly Asn Ile Arg  
       210                  215                  220  
 Trp Glu Leu Ala Gly Thr Leu Leu Leu Val Trp Val Leu Cys Tyr Phe  
       225                  230                  235                  240  
 Cys Ile Trp Lys Gly Val Arg Trp Thr Gly Lys Val Val Tyr Phe Thr  
           245                  250                  255  
 Ala Leu Phe Pro Tyr Phe Leu Leu Thr Val Leu Leu Ile Arg Gly Ile  
       260                  265                  270

Thr	Leu	Pro	Gly	Ala	Met	Glu	Gly	Ile	Lys	Phe	Tyr	Val	Met	Pro	Asn	275	280	285
Met	Ser	Lys	Leu	Leu	Glu	Ser	Glu	Val	Trp	Ile	Asp	Ala	Val	Thr	Gln	290	295	300
Ile	Phe	Phe	Ser	Tyr	Gly	Leu	Gly	Leu	Gly	Thr	Leu	Val	Ala	Leu	Gly	305	310	315
Ser	Tyr	Asn	Lys	Phe	Thr	Asn	Asn	Val	Tyr	Lys	Asp	Ala	Leu	Ile	Val	325	330	335
Cys	Ser	Val	Asn	Ser	Ser	Thr	Ser	Met	Phe	Ala	Gly	Phe	Val	Ile	Phe	340	345	350
Ser	Val	Val	Gly	Phe	Met	Ala	His	Glu	Gln	Gln	Arg	Pro	Val	Ala	Glu	355	360	365
Val	Ala	Ala	Ser	Gly	Pro	Gly	Leu	Ala	Phe	Leu	Ala	Tyr	Pro	Ser	Ala	370	375	380
Val	Leu	Gln	Leu	Pro	Gly	Ala	Pro	Leu	Trp	Ser	Cys	Leu	Phe	Phe	Phe	385	390	395
Met	Leu	Leu	Leu	Ile	Gly	Leu	Asp	Ser	Gln	Phe	Cys	Thr	Met	Glu	Gly	405	410	415
Phe	Ile	Thr	Ala	Val	Ile	Asp	Glu	Trp	Pro	Lys	Leu	Leu	Arg	Arg	Arg	420	425	430
Lys	Glu	Ile	Phe	Ile	Ala	Ile	Thr	Cys	Ile	Ile	Ser	Tyr	Leu	Val	Gly	435	440	445
Leu	Ser	Cys	Ile	Ser	Glu	Gly	Gly	Met	Tyr	Val	Phe	Gln	Ile	Leu	Asp	450	455	460
Ser	Tyr	Ala	Val	Ser	Gly	Phe	Cys	Leu	Leu	Phe	Leu	Ile	Phe	Phe	Glu	465	470	475
Cys	Val	Ser	Ile	Ser	Trp	Ala	Phe	Gly	Val	Asn	Arg	Phe	Tyr	Asp	Gly	485	490	495
Ile	Lys	Glu	Met	Ile	Gly	Tyr	Tyr	Pro	Thr	Ile	Trp	Trp	Lys	Phe	Cys	500	505	510
Trp	Val	Gly	Phe	Thr	Pro	Ala	Ile	Cys	Ile	Ser	Val	Phe	Ile	Phe	Asn	515	520	525
Leu	Val	Gln	Trp	Thr	Pro	Ile	Lys	Tyr	Met	Asn	Tyr	Glu	Tyr	Pro	Trp	530	535	540
Trp	Ser	His	Ala	Phe	Gly	Trp	Phe	Thr	Ala	Leu	Ser	Ser	Met	Leu	Cys	545	550	555
Ile	Pro	Gly	Tyr	Met	Ile	Tyr	Leu	Trp	Arg	Val	Thr	Pro	Gly	Thr	Trp	565	570	575
Gln	Glu	Lys	Phe	His	Lys	Ile	Val	Arg	Ile	Pro	Glu	Asp	Val	Pro	Ser	580	585	590

Leu Arg Thr Lys Met  
595

<210> 15  
<211> 2529  
<212> DNA  
<213> Aedes aegypti  
  
<220>  
<223> LAT transporter

<400> 15  
tgcaaatcca gttcaacgag cgcgacgagc aactgcgaat ccagtttcat tccaagtgcg 60  
ataaaagtca gttgattcag aaagaacggt aggcgccaaa atggtactga aacaacgggg 120  
agcggccata gagctacact ctccctacgga ggatgtgctg gtcagtccgg gaaccgagag 180  
tttgccaccg atcgaaaatg gagccatcgc cggttccggg acgattgatg gcggcggagg 240  
aaacgaacgt gtcaaaatga aaaaagaact ggggctgctg gaaggagtgg ccatcatctt 300  
gggtattatc ttcggctcgg gaattttcat ctgcgccgaag ggtgtgcttc aggagggttg 360  
cgccgtgggg acttcgctgg tcatttgggt gacgtgcggg ttgctgtcga tgattggcgc 420  
gctgtgctat gcagaactgg gcacggcgat accgaaatcc ggtggcgatt atgcttacat 480  
ttatgaggct tatggccac ttccggcggt cctgtatctt tgggacgcaa cgtgatatt 540  
tgtaccgagt acgaacgcca tcatgggact taccttcgcc agctatgtgt tccaaccgct 600  
gtttgcggg ccgatgttccg ttcccacgat agggctgcag ttgtttgccg ccgtgacgat 660  
atgtttgctc acgtacatca atgcttacga cgtccgggtg acgacaaaa tgcagaatgt 720  
gttcatgttc accaaaatcg gtgctctggt gctggctatc atcgttggtg tgggtgtggat 780  
gtcgtctcgg ggaacggaga actttgagaa cgccttcgag aacacggaaa ccgaccccg 840  
caagctggcg gtggcattct attccggtat cttctcgtat gctggatgga attacttgaa 900  
cttcatgacg gaggagcttc gtgaccgcta caagaacctg ccccgagcga tctacatctc 960  
tctcccggtg gtcaccggta tctacgtgct ggccaacatg gcttacgttg cagttctatc 1020  
gccgcagcag attctctcat cggatgctat cgccgtgaca ttcgcccaaga aagccatggg 1080  
ctggggtgcc ttcgtgatgc ccatcctggt agctatttcg gccttcgggtg gtctctccgt 1140  
gcacatcatg acctcatcgc gaatgtgctt cgtcggggcc cgcaacggac acatgccgga 1200  
gatcctcttc cacatcaacg tcaatcggtta cacttcgatg ccgtcgtggtg tgttctctg 1260  
cctcctatcg ttgctgtacc tattcatcag cgacgtgtac gtctgatca cctacagcag 1320  
tategtcgag tcgttcttca tcatgctctc ggtgagtgcg gttctgtact tccgctacac 1380  
ccgaccggac atcaaccggc cgatcaagggt ccaactgtgg gtcccaacgc tgtttgtcat 1440  
catctgtgcg ttctgatcgt tgggtcccgt ctacgtggca ccgtacgaag tgggcatggg 1500  
tgtcctctcg acgctggccg gtattcccgt gtactacgtc ggtgtggcgt ggaagaacaa 1560  
gccggaatcc ttcgagaacg tcctgcgccg ggcgacacag ttctgccaga agatgttcat 1620  
gacggccaaa gaggaaaatg atgacgagga atgagaggag catgcccggt aatgtacagc 1680  
ttacagtttt aattagtagt gccgacgcaa agtgatagta ggtttgacta ttttttaatt 1740  
agttaacgtg accaaacaaa atttttattc tcggacgaaa tttaaatctc aatcgttata 1800  
gatctgtttt catcaattga caaaatttta gatcagtgc aaatatgttt ggagtcgatt 1860  
ttggatcata cactcccacg gttttttgtt gcgatgaaat cgcgaaatca ttagtcaaaa 1920  
ttgaaaattt actttatgtt tccacatgtg cgtccagttc cagtacttac aatttaagtc 1980  
agacaaatca aataaaaaatg tactttataa tctccattgc attttgtgta agagtctcca 2040  
tcaacgaacc ggaaaccgaa gtgtcccgggt ccggtatgat acttcttcat aagaagtcaa 2100  
gcaaacgaaa gtgtagaata ttttactca atcctataat agaccaatga ggtttaagct 2160  
aaaaccaata cgcttttgag cttttctcta tcaaacatca caccgatcaa ttagaatctc 2220  
atgctcatgc tatatgttgt cggacttgcg gcgccagatt gtaccaagaa ctggtttgat 2280  
atctagaagc aaaacatctc actgaaagag ggaaagacaa aagataagac tattatacat 2340  
acacaaacac tcgaataaag caaactgctc gtagttagcc gttgaagtta gcatagtgcg 2400  
agtatggaag ttttgaatag aaacgtaaga gattgaataa catagggttaa gtttgcaagc 2460  
aatgccgaca aataccatt atgataataa accatgctag attttttgtt aaaaaaaaaa 2520  
aaaaaaaaa 2529

<210> 16  
 <211> 517  
 <212> PRT  
 <213> Aedes aegypti

<220>  
 <223> LAT transporter

<400> 16  
 Met Val Leu Lys Gln Arg Gly Ala Ala Ile Glu Leu His Ser Pro Thr  
   1                  5                  10                  15  
 Glu Asp Val Leu Val Ser Pro Gly Thr Glu Ser Leu Pro Pro Ile Glu  
                   20                  25                  30  
 Asn Gly Ala Ile Ala Gly Ser Gly Thr Ile Asp Gly Gly Gly Gly Asn  
           35                  40                  45  
 Glu Arg Val Lys Met Lys Lys Glu Leu Gly Leu Leu Glu Gly Val Ala  
           50                  55                  60  
 Ile Ile Leu Gly Ile Ile Phe Gly Ser Gly Ile Phe Ile Ser Pro Lys  
   65                  70                  75                  80  
 Gly Val Leu Gln Glu Val Gly Ala Val Gly Thr Ser Leu Val Ile Trp  
                   85                  90                  95  
 Val Thr Cys Gly Leu Leu Ser Met Ile Gly Ala Leu Cys Tyr Ala Glu  
                   100                  105                  110  
 Leu Gly Thr Ala Ile Pro Lys Ser Gly Gly Asp Tyr Ala Tyr Ile Tyr  
           115                  120                  125  
 Glu Ala Tyr Gly Pro Leu Ser Ala Phe Leu Tyr Leu Trp Asp Ala Thr  
           130                  135                  140  
 Val Ile Phe Val Pro Ser Thr Asn Ala Ile Met Gly Leu Thr Phe Ala  
   145                  150                  155                  160  
 Ser Tyr Val Phe Gln Pro Leu Phe Ala Ala Gly Cys Ser Val Pro Thr  
                   165                  170                  175  
 Ile Gly Leu Gln Leu Phe Ala Ala Val Thr Ile Cys Leu Leu Thr Tyr  
           180                  185                  190  
 Ile Asn Ala Tyr Asp Val Arg Val Thr Thr Lys Met Gln Asn Val Phe  
           195                  200                  205  
 Met Phe Thr Lys Ile Gly Ala Leu Val Leu Val Ile Ile Val Gly Val  
           210                  215                  220  
 Val Trp Met Ser Leu Gly Gly Thr Glu Asn Phe Glu Asn Ala Phe Glu  
   225                  230                  235                  240  
 Asn Thr Glu Thr Asp Pro Gly Lys Leu Ala Val Ala Phe Tyr Ser Gly  
                   245                  250                  255  
 Ile Phe Ser Tyr Ala Gly Trp Asn Tyr Leu Asn Phe Met Thr Glu Glu  
           260                  265                  270



Leu Arg Asp Pro Tyr Lys Asn Leu Pro Arg Ala Ile Tyr Ile Ser Leu  
 275 280 285  
 Pro Leu Val Thr Gly Ile Tyr Val Leu Ala Asn Met Ala Tyr Val Ala  
 290 295 300  
 Val Leu Ser Pro Gln Gln Ile Leu Ser Ser Asp Ala Ile Ala Val Thr  
 305 310 315 320  
 Phe Ala Gln Lys Ala Met Gly Trp Gly Ala Phe Val Met Pro Ile Leu  
 325 330 335  
 Val Ala Ile Ser Ala Phe Gly Gly Leu Ser Val His Ile Met Thr Ser  
 340 345 350  
 Ser Arg Met Cys Phe Val Gly Ala Arg Asn Gly His Met Pro Glu Ile  
 355 360 365  
 Leu Phe His Ile Asn Val Asn Arg Tyr Thr Ser Met Pro Ser Leu Val  
 370 375 380  
 Phe Leu Cys Leu Leu Ser Leu Leu Tyr Leu Phe Ile Ser Asp Val Tyr  
 385 390 395 400  
 Val Leu Ile Thr Tyr Ser Ser Ile Val Glu Ser Phe Phe Ile Met Leu  
 405 410 415  
 Ser Val Ser Ala Val Leu Tyr Phe Arg Tyr Thr Arg Pro Asp Ile Asn  
 420 425 430  
 Arg Pro Ile Lys Val Gln Leu Trp Val Pro Thr Leu Phe Val Ile Ile  
 435 440 445  
 Cys Ala Phe Leu Ile Val Val Pro Cys Tyr Val Ala Pro Tyr Glu Val  
 450 455 460  
 Gly Met Gly Val Leu Leu Thr Leu Ala Gly Ile Pro Val Tyr Tyr Val  
 465 470 475 480  
 Gly Val Ala Trp Lys Asn Lys Pro Glu Ser Phe Glu Asn Val Leu Arg  
 485 490 495  
 Arg Ala Thr Gln Phe Cys Gln Lys Met Phe Met Thr Ala Lys Glu Glu  
 500 505 510  
 Asn Asp Asp Glu Glu  
 515

<210> 17

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:1S forward  
degenerate primer for NTTs (A69)

<220>  
<221> modified\_base  
<222> (19)  
<223> n = i

<220>  
<221> modified\_base  
<222> (25)  
<223> n = i

<220>  
<221> modified\_base  
<222> (31)  
<223> n = g, a, c or t

<400> 17  
cggaattctg gscaayrtnt ggmgttycc nta

33

<210> 18  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:4A reverse  
degenerate primer for NTTs (A67)

<220>  
<221> modified\_base  
<222> (24)..(25)  
<223> n = i

<220>  
<221> modified\_base  
<222> (28)  
<223> n = i

<220>  
<221> modified\_base  
<222> (34)  
<223> n = g, a, c or t

<400> 18  
gccaaagcttg aagaagatyt grgngcngc rtcnabcca

39

<210> 19  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:2S reverse  
degenerate primer for NTTs (A70)

<220>  
<221> modified\_base  
<222> (16)  
<223> n = i

```

<220>
<221> modified_base
<222> (19)
<223> n = i

<220>
<221> modified_base
<222> (22)
<223> n = i

<220>
<221> modified_base
<222> (25)
<223> n = g, a, c or t

<400> 19
ctccatggar aayggnggng gngcntt

```

27

```

<210> 20
<211> 30
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:3A reverse
degenerate primer for NTTs (A68)

```

```

<220>
<221> modified_base
<222> (13)
<223> n = i

```

```

<220>
<221> modified_base
<222> (16)
<223> n = i

```

```

<220>
<221> modified_base
<222> (19)
<223> n = i

```

```

<220>
<221> modified_base
<222> (22)
<223> n = i

```

```

<220>
<221> modified_base
<222> (25)
<223> n = g, a, c or t

```

```

<220>
<221> modified_base
<222> (28)
<223> n = g, a, c or t

```

```

<400> 20
ggcgagctcg gncncnggna gngtnrncnc

```

30